JOURNAL OF THEORETICAL BIOLOGY

Co-Chief Editors: S. A. KAUFFMAN
L. WOLPERT

Editorial Board: J. BONNER
B. CHARLESWORTH
P. F. COOK
A. CORNISH-BOWDEN
J. COWAN
F. DYSON
D. GARFINKEL
M. E. GILPIN
L. GLASS
A. GOLDBETER
B. GOODWIN
P. W. HEDRICK
M. KARPLUS
T. B. L. KIRKWOOD
Y. KOBATAKE
R. C. LEWONTIN
W. R. LIEB
R. B. LUFTIG
R. M. MAY
J. MAYNARD SMITH
J. D. MURRAY
T. OHTA
H. H. PATTEE
J. RINZEL
P. SCHUSTER
J. H. STEINBACH
T. TAKENAKA
M. VOLKENSTEIN
J. Z. YOUNG

VOLUME 134
September–October 1988

ACADEMIC PRESS

London San Diego New York Boston
Sydney Tokyo Toronto

Copyright © 1988, by Academic Press Limited

ALL RIGHTS RESERVED

No part of this volume may be reproduced in any
form, by photostat, microfilm, or any other means,
without written permission from the publishers.

Printed in Great Britain

Contents for Volume 134

Number 1, 7 September 1988

CORNISH-BOWDEN, A., Significance of the Purine-Pyrimidine Motif Present in Most Gene Groups 1

GOEL, N. S. and THOMPSON, R. L., Movable Finite Automata (MFA) Models for Biological Systems II: Protein Biosynthesis 9

CURNOW, R. N., The Use of Markov Chain Models in Studying the Evolution of the Proteins 51

HARPER, D. G. and BLAKE, R. W., Energetics of Piscivorous Predator-Prey Interactions 59

GROVER, N. B., Surface-Limited Growth: A Model for the Synchronization of a Growing Bacterial Culture through Periodic Starvation . . 77

ROWE, G. W., To Each Genotype a Separate Strategy—A Dynamic Game Theory Model of a General Diploid System 89

HASTINGS, A., Dependence of Expected Heterozygosity on Locus Number with Stabilizing Selection and Drift 103

BULLIMAN, B. T. and KUCHEL, P. W., A Series Expression for the Surface Area of an Ellipsoid and its Application to the Computation of the Surface Area of Avian Erythrocytes 113

LETTER TO THE EDITOR

WEINBERGER, E., A More Rigorous Derivation of Some Properties of Uncorrelated Fitness Landscapes 125

ANNOUNCEMENTS 131

ERRATA 133

Number 2, 21 September 1988

MADER, A., A Transcription-Translation Activation Feedback Circuit as a Function of Protein Degradation, with the Quality of Protein Mass Adaptation Related to the Average Functional Load 135

FILIPSKI, J., Why the Rate of Silent Codon Substitutions is Variable Within a Vertebrate's Genome 159

PEDEMONTE, C. H., Kinetic Mechanism of Inhibition of the Na^+-Pump and some of its Partial Reactions by External Na^+ (Na_o^+) 165

NEWMAN, S. A., FRISCH, H. L. and PERCUS, J. K., On the Stationary State Analysis of Reaction-Diffusion Mechanisms for Biological Pattern Formation 183

NAGANO, K., HAREL, M. and TAKEZAWA, M., Prediction of Three-Dimensional Structure of *Escherichia coli* Ribosomal RNA . . 199

HAIG, D. and WESTOBY, M., A Model for the Origin of Heterospory . 257

Number 3, 7 October 1988

JOB, D., SOULIE, J. M. and JOB, C., Potential Memory and Hysteretic Effects in Transcription 273

HAGGARTY, P., MCGAW, B. A. and FRANKLIN, M. F., Measurement of Fractionated Water Loss and CO_2 Production using Triply Labelled Water 291

OMHOLT, S. W., Drone Production in Honeybee Colonies: Controlled by a Long-lasting Inhibitory Pheromone from the Drones? 309

CHELA-FLORES, J., LIQUORI, A. M. and FLORIO, A. A Kinetic Thermodynamic Phenomenological Approach to Genetic Expression of Heat-Shock Proteins 319

GENONI, G. P., Sensory Discrimination and the Incipient Advantage of Mutations 327

DUFTON, M. J. and BLADON, P., A Method for Detecting Centres of Natural Selection in Protein Structures: Potential for Predicting the Location of Functional Areas 331

NORRIS, V., SEROR, S. J., CASAREGOLA, S. and HOLLAND, I. B., A Single Calcium Flux Triggers Chromosome Replication, Segregation and Septation in Bacteria: a Model 341

KEMP, G. J., BEVINGTON, A. and RUSSELL, R. G. G., Theoretical Interpretation of Isotope Labelling Experiments in Cells in which the Label is Chemically Incorporated: The Example of Orthophosphate 351

SAVAGE, J. R. K. and PAPWORTH, D. G., A Method for Comparing DNA Replication Programmes at the Level of the Chromosome Bands . 365

BUXBAUM, R. E. and HEIDEMANN, S. R., A Thermodynamic Model for Force Integration and Microtubule Assembly During Axonal Elongation . 379

JANOVY, JR., J. and KUTISH, G. W., A Model of Encounters Between Host and Parasite Populations 391

NUNOGAKI, K. and KASAI, M., The H^+/OH^- Flux Localizes Around the Channel Mouth in Buffered Solution 403

ANNOUNCEMENT 417

Number 4, 21 October 1988

FERNÁNDEZ, A., Stochastic Dynamical Constraints in *de novo* RNA Replication 419

GARCÍA-TEJEDOR, A., SANZ-NUÑO, J. C., OLARREA, J., JAVIER DE LA RUBIA, F. and MONTERO, F., Influence of the Hypercycle on the Error Threshold: A Stochastic Approach 431

VILA, J. and ALESSANDRINI, J. L., Adsorption of an Ionic Homopolypeptide to a Flat Surface Induced by pH Change 445

GIERSCH, C., Control Analysis of Biochemical Pathways: A Novel Procedure for Calculating Control Coefficients, and an Additional Theorem for Branched Pathways 451

KOCH, A. L., Partition of Autolysins Between the Medium, the Internal Part of the Wall, and the Surface of the Wall of Gram-positive Rods . 463

MULLER, M. and VERHAGEN, J. H. G., A New Quantitative Model of Total Endolymph Flow in the System of Semicircular Ducts 473

MULLER, M. and VERHAGEN, J. H. G., A Mathematical Approach Enabling the Calculation of the Total Endolymph Flow in the Semicircular Ducts . 503

LAM, G. K. Y., The Combined Effects of Mixtures of Ionizing Radiations 531

SACHS, T., Epigenetic Selection: An Alternative Mechanism of Pattern Formation 547

LETTERS TO THE EDITOR

SZATHMÁRY, E., A Hypercyclic Illusion 561

MAGUIRE, M. P., Crossover Site Determination and Interference . 565

Index to Volume 134

Adsorption of an ionic homopolypeptide to a flat surface induced by pH change, 445
ALESSANDRINI, J. L. (see VILA, J.), 445
Assembly, microtubule, during axonal elongation, a thermodynamic model for force integration and, 379
Autolysins, partition between the medium, the internal part of the wall, and the surface of the wall of Gram-positive rods, 463
Avian erythrocytes, computation of surface area using a series expression for the surface area of an ellipsoid, 113
Axonal elongation, a thermodynamic model for force integration and microtubule assembly during, 379

Bacteria, a single calcium flux triggers chromosome replication, segregation and septation in; a model, 341
Bacterial culture, growing, a model for the synchronization of, through periodic starvation, 77
BEVINGTON, A. (see KEMP, G. J.), 351
Biochemical pathways, control analysis: a novel procedure for calculating control coefficients, and an additional theorem for branched pathways, 451
Biological systems, movable finite automata (MFA) models for; protein biosynthesis, 9
Biosynthesis, protein: movable finite automata (MFA) models for biological systems, 9
BLADON, P. (see DUFTON, M. J.), 331
BLAKE, R. W. (see HARPER, D. G.), 59
Buffered solution, the H^+/OH^- flux localizes around the channel mouth in, 403
BULLIMAN, B. T. and KUCHEL, P. W., A series expression for the surface area of an ellipsoid and its application to the computation of the surface area of avian erythocytes, 113
BUXBAUM, R. E. and HEIDEMANN, S. R., A thermodynamic model for force integration and microtubule assembly during axonal elongation, 379

Calcium flux, single, triggers chromosome replication, segregation and septation in bacteria: a model, 341
CO_2 production, measurement of fractionated water loss and, using triply labelled water, 291
CASAREGOLA, S. (see NORRIS, V.), 341
Cells in which the label is chemically incorporated, theoretical interpretation of isotope labelling experiments in; example of orthophosphate, 351
Channel mouth, the H^+/OH^- flux localizes around, in buffered solution, 403
CHELA-FLORES, J., LIQUORI, A. M. and FLORIO, A., A kinetic thermodynamic phenomenological approach to genetic expression of heat-shock proteins, 319
Chromosome bands, a method for comparing DNA replication programmes at the level of, 365
Chromosome replication, segregation and septation in bacteria, triggered by a single calcium flux; a model, 341
Control analysis of biochemical pathways: a novel procedure for calculating control coefficients, and an additional theorem for branched pathways, 451
CORNISH-BOWDEN, A., Significance of the purine-pyrimidine motif present in most gene groups, 1
Crossover site determination and interference (letter), 565
CURNOW, R. N., The use of Markov chain models in studying the evolution of the proteins, 51

Diploid system, general, a dynamic game theory model of; to each genotype a separate strategy, 89
DNA replication programmes at the level of the chromosome bands, a method for comparing, 365
Drone production in honeybee colonies: controlled by a long-lasting pheromone from the drones?, 309
Ducts, semicircular, a mathematical approach enabling the calculation of the total endolymph flow in, 503
Ducts, semicircular, a new quantitative model of total endolymph flow in the system of, 473
DUFTON, M. J. and BLADON, P., A method for detecting centres of natural selection in protein structures: potential for predicting the location of functional areas, 331
Dynamic game theory model of a general diploid system; to each genotype a separate strategy, 89

Ellipsoid, a series expression for the surface area: application to computation of the surface area of avian erythrocytes, 113
Encounters between host and parasite populations, a model of, 391
Endolymph flow in the semicircular ducts, a mathematical approach enabling the calculation of, 503
Endolymph flow in the system of semicircular ducts, a new quantitative model, 473
Energetics of piscivorous predator–prey interactions, 59
Epigenetic selection: an alternative mechanism of pattern formation, 547
Error threshold, stochastic approach to influence of the hypercycle on, 431
Erythrocytes, avian, computation of surface area using a series expression for the surface area of an ellipsoid, 113
Escherichia coli ribosomal RNA, prediction of three-dimensional structure, 199
Evolution of the proteins, use of Markov chain models in study of, 51

FERNÁNDEZ, A., Stochastic dynamical constraints in *de novo* RNA replication, 419
FILIPSKI, J., Why the rate of silent codon substitutions is variable within a vertebrate's genome, 159
Fitness landscapes, uncorrelated, a more rigorous derivation of some properties of (letter), 125
FLORIO, A. (see CHELA-FLORES, J.), 319
Force integration and microtubule assembly during axonal elongation, a thermodynamic model for, 379
Fractionated water loss and CO_2 production, measurement using triply labelled water, 291
FRANKLIN, M. F. (see HAGGARTY, P.), 291
FRISCH, H. L. (see NEWMAN, S. A.), 183

Game theory model of a general diploid system; to each genotype a separate strategy, 89
GARCÍA-TEJEDOR, A., SANZ-NUÑO, J. C., OLARREA, J., JAVIER DE LA RUBIA, F. and MONTERO, F., Influence of the hypercycle on the error threshold: a stochastic approach, 431
Gene groups, most, significance of the purine-pyrimidine motif present in, 1
Genetic expression of heat-shock proteins, a kinetic thermodynamic phenomenological approach, 319
Genome, vertebrate's, why the rate of silent codon substitutions is variable within, 159
GENONI, G. P., Sensory discrimination and the incipient advantage of mutations, 327
Genotype, to each a separate strategy; a dynamic game theory model of a general diploid system, 89
GIERSCH, C., Control analysis of biochemical pathways: a novel procedure for calculating control coefficients, and an additional theorem for branched pathways, 451
GOEL, N. S. and THOMPSON, R. L., Movable finite automata (MFA) models for biological systems II. Protein biosynthesis, 9

Gram-positive rods, partition of autolysins between the medium, the internal part of the wall, and the surface of the wall of, 463
GROVER, N. B., Surface-limited growth: a model for the synchronization of a growing bacterial culture through periodic starvation, 77
Growth, surface-limited; a model for the synchronization of a growing bacterial culture through periodic starvation, 77

HAGGARTY, P., MCGAW, B. A. and FRANKLIN, M. F., Measurement of fractionated water loss and CO_2 production using triply labelled water, 291
HAIG, D. and WESTOBY, A., A model for the origin of heterospory, 257
HAREL, M. (see NAGANO, K.), 199
HARPER, D. G. and BLAKE, R. W., Energetics of piscivorous predator–prey interactions, 59
HASTINGS, A., Dependence of expected heterozygosity on locus number with stabilizing selection and drift, 103
Heat-shock proteins, a kinetic thermodynamic phenomenological approach to genetic expression of, 319
HEIDEMANN, S. R. (see BUXBAUM, R. E.), 379
Heterospory, a model for the origin of, 257
Heterozygosity, expected, dependence on locus number with stabilizing selection and drift, 103
HOLLAND, I. B. (see NORRIS, V.), 341
Homopolypeptide, ionic, adsorption to a flat surface induced by pH change, 445
Honeybee colonies, drone production in; controlled by a long-lasting pheromone from the drones?, 309
Host and parasite populations, a model of encounters between, 381
H^+/OH^- flux localizes around the channel mouth in buffered solution, 403
Hypercycle, influence on the error threshold; a stochastic approach, 431
Hypercyclic illusion (letter), 561
Hysteretic effects in transcription, 273

Interference, crossover site determination and (letter), 565
Ionizing radiations, the combined effects of mixtures of, 531
Isotope labelling experiments in cells in which the label is chemically incorporated, theoretical interpretation of; example of orthophosphate, 351

JANOVY, J. and KUTISH, G. W., A model of encounters between host and parasite populations, 391
JAVIER DE LA RUBIA, F. (see GARCÍA-TEJEDOR, A.), 431
JOB, C. (see JOB, D.), 273
JOB, D., SOULIE, J. M. and JOB, C., Potential memory and hysteretic effects in transcription, 273

KASAI, M. (see NUNOGAKI, K.), 403
KEMP, G. J., BEVINGTON, A. and RUSSELL, R. G. G., Theoretical interpretation of isotope labelling experiments in cells in which the label is chemically incorporated: the example of orthophosphate, 351
Kinetic mechanism of inhibition of the Na^+-pump and some of its partial reactions by external Na^+ (Na_0^+), 165
Kinetic thermodynamic phenomenological approach to genetic expression of heat-shock proteins, 319
KOCH, A. L., Partition of autolysins between the medium, the internal part of the wall, and the surface of the wall of Gram-positive rods, 463
KUCHEL, P. W. (see BULLIMAN, B. T.), 113
KUTISH, G. W. (see JANOVY, J.), 391

LAM, G. K. Y., The combined effects of mixtures of ionizing radiations, 531
Landscapes, fitness, uncorrelated, a more rigorous derivation of some properties of (letter), 125
LIQUORI, A. M. (see CHELA-FLORES, J.), 319
Locus number, dependence of expected heterozygosity on, with stabilizing selection and drift, 103

MCGAW, B. A. (see HAGGARTY, P.), 291
MADER, A., A transcription-translation activation feedback circuit as a function of protein degradation, with the quality of protein mass adaptation related to the average functional load, 135
MAGUIRE, M. P., Crossover site determination and interference (letter), 565
Markov chain models: use in studying the evolution of the proteins, 51
Memory and hysteretic effects in transcription, 273
Microtubule assembly during axonal elongation, a thermodynamic model for force integration and, 379
MONTERO, F. (see GARCÍA-TEJEDOR, A.), 431
Movable finite automata (MFA) models for biological systems; protein biosynthesis, 9
MULLER, M. and VERHAGEN, J. H. G., A mathematical approach enabling the calculation of the total endolymph flow in the semicircular ducts, 503
MULLER, M. and VERHAGEN, J. H. G., A new quantitative model of total endolymph flow in the system of semicircular ducts, 473
Mutations, sensory discrimination and the incipient advantage of, 327

NAGANO, K., HAREL, M. and TAKEZAWA, M., Prediction of three-dimensional structure of *Escherichia coli* ribosomal RNA, 199
Na^+-pump and some of its partial reactions, kinetic mechanism of inhibition by external Na^+ (Na_0^+), 165
NEWMAN, S. A., FRISCH, H. L. and PERCUS, J. K., On the stationary state analysis of reaction-diffusion mechanisms for biological pattern formation, 183
NORRIS, V., SEROR, S. J., CASAREGOLA, S. and HOLLAND, I. B., A single calcium flux triggers chromosome replication, segregation and septation in bacteria: a model, 341
NUNOGAKI, K. and KASAI, M., The H^+/OH^- flux localizes around the channel mouth in buffered solution, 403

OLARREA, J. (see GARCÍA-TEJEDOR, A.), 431
OMHOLT, S. W., Drone production in honeybee colonies: controlled by a long-lasting inhibitory pheromone from the drones?, 309
Orthophosphate: theoretical interpretation of isotope labelling experiments in cells in which the label is chemically incorporated, 351

PAPWORTH, D. G. (see SAVAGE, J. R. K.), 365
Parasite populations, a model of encounters between host and, 391
Pathways, biochemical, control analysis; a novel procedure for calculating control coefficients, and an additional theorem for branched pathways, 451
Pattern formation, an alternative mechanism; epigenetic selection, 547
Pattern formation, biological, the stationary state analysis of reaction-diffusion mechanisms for, 183
PEDEMONTE, C. H., Kinetic mechanism of inhibition of the Na^+-pump and some of its partial reactions by external Na^+ (Na_0^+), 165
PERCUS, J. K. (see NEWMAN, S. A.), 183
pH change, adsorption of an atomic homopolypeptide to a flat surface induced by, 445
Pheromone, long-lasting, and control of drone production in honeybee colonies, 309
Piscivorous predator–prey interactions, energetics of, 59

Predator–prey interactions, piscivorous, energetics of, 59
Protein biosynthesis: movable finite automata (MFA) models for biological systems, 9
Protein degradation, a transcription-translation activation feedback circuit as a function of, with the quality of protein mass adaptation related to the average functional load, 135
Proteins, heat-shock, a kinetic thermodynamic phenomenological approach to genetic expression of, 319
Proteins, the use of Markov chain models in studying the evolution of, 51
Protein structures, a method for detecting centres of natural selection in; potential for predicting the location of functional areas, 331
Purine-pyrimidine motif present in most gene groups, significance of, 1

Reaction-diffusion mechanisms for biological pattern formation, the stationary state analysis of, 183
Replication, DNA, programmes at the level of the chromosone bands, a method for comparing, 365
Replication, RNA, *de novo*, stochastic dynamical constraints in, 419
Replication, segregation and septation in bacteria, triggered by a single calcium flux; a model, 341
Ribosomal RNA, *Escherichia coli*, prediction of three-dimensional structure of, 199
RNA replication, *de novo*, stochastic dynamical constraints in, 419
RNA, ribosomal, *Escherichia coli*, prediction of three-dimensional structure of, 199
Rods, Gram-positive, partition of autolysins between the medium, the internal part of the wall, and the surface of the wall of, 463
ROWE, G. W., To each genotype a separate strategy—a dynamic game theory model of a general diploid system, 89
RUSSELL, R. G. G. (see KEMP, G. J.), 351

SACHS, T., Epigenetic selection: an alternative mechanism of pattern formation, 547
SANZ-NUÑO, J. C. (see GARCÍA-TEJEDOR, A.), 431
SAVAGE, J. R. K. and PAPWORTH, D. G., A method for comparing DNA replication programmes at the level of the chromosome bands, 365
Selection centres in protein structures, a method for detection of; potential for predicting the location of functional areas, 331
Selection, epigenetic: an alternative mechanism of pattern formation, 547
Selection, stabilizing, and drift, dependence of expected heterozygosity on locus number with, 103
Sensory discrimination and the incipient advantage of mutations, 327
Septation, a single calcium flux triggers chromosome replication, segregation and; in bacteria; a model, 341
SEROR, S. J. (see NORRIS, V.), 341
Silent codon substitution rate, why it is variable within a vertebrate's genome, 159
SOULIE, J. M. (see JOB, D.), 273
Stationary state analysis of reaction-diffusion mechanisms for biological pattern formation, 183
Starvation, periodic, a model for the synchronization of a growing bacterial culture through, 77
Stochastic approach to influence of the hypercycle on the error threshold, 431
Stochastic dynamical constraints in *de novo* RNA replication, 419
Structures, protein, a method for detecting centres of natural selection in; potential for predicting the location of functional areas, 331
Structure, three-dimensional, of *Escherichia coli* ribosomal RNA, prediction of, 199
Surface area of an ellipsoid, series expression for; application to computation of the surface area of avian erythrocytes, 113
Surface, flat, adsorption of an ionic homopolypeptide to, induced by pH change, 445

Surface-limited growth: a model for the synchronization of a growing bacterial culture through periodic starvation, 77
Synchronization of a growing bacterial culture through periodic starvation; a model of surface-limited growth, 77
SZATHMÁRY, E., A hypercyclic illusion (letter), 561

TAKEZAWA, M. (see NAGANO, K.), 199
Thermodynamic kinetic phenomenological approach to genetic expression of heat-shock proteins, 319
Thermodynamic model for force integration and microtubule assembly during axonal elongation, 379
THOMPSON, R. L. (see GOEL, N. S.), 9
Transcription, potential memory and hysteretic effects in, 273
Transcription-translation activation feedback circuit as a function of protein degradation, with the quality of protein mass adaptation related to the average functional load, 135

VERHAGEN, J. H. G. (see MULLER, M.), 473, 503
Vertebrate's genome, why the rate of silent codon substitution is variable within, 159
VILA, J. and ALESSANDRINI, J. L., Adsorption of an ionic homopolypeptide to a flat surface induced by pH change, 445

Water, triply labelled, use in measurement of fractionated water loss and CO_2 production, 291
WEINBERGER, E., A more rigorous derivation of some properties of uncorrelated fitness landscapes (letter), 125
WESTOBY, A. (see HAIG, D.), 257